RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/018, 105 A_

Source: _IFW16_

Date Processed by STIC: _12/13/2005_

ENTERED

RAW SEQUENCE LISTING   DATE: 12/13/2005
PATENT APPLICATION: US/10/018,105A   TIME: 16:17:30

Input Set : **E:\substitute SEQLIST (10182-015-999).TXT**
Output Set: **N:\CRF4\12132005\J018105A.raw**

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 4 <110> APPLICANT: MYCOTA BIOSCIENCES INC.
 5       ROEMER, Terry
 6       BUSSEY, Howard
 7       DAVISON, John
 9 <120> TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
10       SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
11       DISCOVERY
13 <130> FILE REFERENCE: 10182-015-999 (originally 12875.3)
15 <140> CURRENT APPLICATION NUMBER: US/10/018,105A
16 <141> CURRENT FILING DATE: 2002-07-15 (371c date 2000-05-05)
18 <150> PRIOR APPLICATION NUMBER: 60/132,878
19 <151> PRIOR FILING DATE: 1999-05-05
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 7558
27 <212> TYPE: DNA
28 <213> ORGANISM: Candida albicans
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (2770)..(7110)
33 <223> OTHER INFORMATION: Candida albicans KRE5
35 <400> SEQUENCE: 1
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38 gccaatttca agatgttgac aaagttgcgt ctatggcact accacctcta ctgggaggat 120
40 gtgtaccctg tattgatcgt ggaggatgtc gagctccaca actgcacgtg ggagtttccg 180
42 ttcacgctat cgcaattcaa ttacaactcc aacatcaggc gacttgtggt gtcgtatgct 240
44 gaaggcaacg cgtttgcggt gtctgaacgg tacagagagt ttttgcaata tggaaacgga 300
46 gaagactttt caagtttgga ggagcttacg gtcactgtgg cgagagggag tctcaacagc 360
48 agcgtgatgt cacggttcat gaacactggc aacttcccga gactaagagc attgcgggtt 420
50 cttgcaaggg aaggcgcata caacctatcg cattggtttg gaaagttgcc gacaaaacag 480
52 tacgttgcgg gtactagaca tgcaggtgga ttacgaagct cgtgaccggg agagagcatt 540
54 gaaggaggcc aatagatact ttccattcct tgatgtgaag atacatagac cataaaagca 600
56 caaggctgcg aaatatatac gcgtatagac tctactaata aacatccaaa ccagagtgaa 660
58 aaaaaaaat acaacacaaa ccagaaaaaa aacaaacgaa ccacttacaa gacccatctc 720
60 taccacaaca ccaatgtact gggtgctact ccttttcgtg tcgatatgca tggccaacac 780
62 ggagacatgc ttggtacggg tgcccgagta ctacaatatt gtaccgcacc cgtcacccat 840
64 atccagggat gccaggttca gtcgcgagct ccatcgtctc aacaccaccc acacagtact 900
66 actagactac cccattggat ctatcgacga ccaggatatg tccaacataa tcacagtcac 960
68 atacgatacc gttgcgcaac cacgatcaac actactagtg cgcgtgaaca actacggaga 1020
70 caatacgttt acgaacggcg acatgctcaa cattaagcta tgctggccgg ccaccatgcc 1080
72 gtacgacttt agcattgacc atgtgtatat gcacagcaac gagttggttg agagtgtgga 1140
74 ggatgagttt gatttgtatg tggcggtcac ctacgagttc catgcctta gttatgacaa 1200
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 76 tgggaggttt ttgcaagaag aaacggcatt gtccttccaa ttgtacgtga acaaattgcc 1260
 78 cagtagattc ttacccattc cattggagtt gtacgaaaca atcgtgtatt tagtagatat 1320
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 82 ggggcagtag tgttgcgtta tattttaagg aaaataaaca aatgatttta tcaagtcgat 1440
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108 tcagagagca aaggctcaag gaattaagca aaccaaagtt tgcgaatgaa agcaaagttt 2220
110 taggactgaa ttcaaaaatt aataaaccta tcggtggctc gccaagggat cttagacagg 2280
112 caattctaga ggcggcagag cgtcggttga gagattcaaa atggtgtcat agtgaaaatg 2340
114 cagaaaccga aagtgttccc aaagaggacg agtacgacac aactcaggtg gagcttatcg 2400
116 gtcctacaga aggtaaacca gttggaacat ttgctaatga tatcattgat ttaacatcgg 2460
118 acactgaaga aactccaatt caacctgata acccgaaacg ccgcatactc cacgagataa 2520
120 ttgatttaac ttcagataca gaagacatag agccaacatc accagaggta atatgtatag 2580
122 attaagttaa atataaaggc aaatatattg ccaatgtaat actcttttaa cagtgttgtt 2640
124 ctcgtgcaag gattaagcac cgaaaaaaaa tatgtggatg cgttgttatt agttttactc 2700
126 tttgcttttt ctgaaaagaa acattaacgt gttctactag tttgtcacac tacgacacaa 2760
128 gtccttgaa atg tca ttt gca agg tat atc tac tac acc att gcg gtt gct 2811
129          Met Ser Phe Ala Arg Tyr Ile Tyr Tyr Thr Ile Ala Val Ala
130          1                5                    10
132 gtt tta tta aat ttt gtc aaa gct act gaa aat aac aat ttt aaa ctt 2859
133 Val Leu Leu Asn Phe Val Lys Ala Thr Glu Asn Asn Asn Phe Lys Leu
134 15                20                    25                    30
136 gaa gtt gaa gcg tca tgg agc aat att gat ttc ctt cct agc ttt ata 2907
137 Glu Val Glu Ala Ser Trp Ser Asn Ile Asp Phe Leu Pro Ser Phe Ile
138                   35                40                    45
140 gag gcc atc gtt ggc ttc aat gac tct ttg tac gaa cag aca att gaa 2955
141 Glu Ala Ile Val Gly Phe Asn Asp Ser Leu Tyr Glu Gln Thr Ile Glu
142                   50                55                    60
144 aca att ttt ggt tta gga gac act gaa gtg gaa tta gaa gat gat gct 3003
145 Thr Ile Phe Gly Leu Gly Asp Thr Glu Val Glu Leu Glu Asp Asp Ala
146             65                70                    75
148 tca gat caa gaa ata tat tct acc gtg atc aac tca tta ggg tta aca 3051
149 Ser Asp Gln Glu Ile Tyr Ser Thr Val Ile Asn Ser Leu Gly Leu Thr
150          80                85                    90
152 gat caa gat ttg gat ttt att aat ttt gat tta acc aac aaa aaa cat 3099
153 Asp Gln Asp Leu Asp Phe Ile Asn Phe Asp Leu Thr Asn Lys Lys His
154 95                    100                    105                    110
156 aca cca aga atc gca gcc cat tac gat cac tat tct gat gtt cta act 3147
157 Thr Pro Arg Ile Ala Ala His Tyr Asp His Tyr Ser Asp Val Leu Thr
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Input Set : E:\substitute SEQLIST (10182-015-999).TXT
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160 aag ttt ggc gat cga ctc aaa agt gaa tgt gca aaa gac tct ttt ggg   3195
161 Lys Phe Gly Asp Arg Leu Lys Ser Glu Cys Ala Lys Asp Ser Phe Gly
162                130                135                140
164 aat gca gtg gaa acg aaa aat ggt caa att caa acg tgg tta cta tat   3243
165 Asn Ala Val Glu Thr Lys Asn Gly Gln Ile Gln Thr Trp Leu Leu Tyr
166            145                150                155
168 aac gat aag ata tat tgt tcg gct aat gat ttg ttt gca tta cga act   3291
169 Asn Asp Lys Ile Tyr Cys Ser Ala Asn Asp Leu Phe Ala Leu Arg Thr
170        160                165                170
172 gat ttg agt tct cat tct aca ctt tta ttt gat agg att att gga aaa   3339
173 Asp Leu Ser Ser His Ser Thr Leu Leu Phe Asp Arg Ile Ile Gly Lys
174 175                180                185                190
176 tca aaa gat gca cct ttg gtg att tta tat gga agc ccg act gag gaa   3387
177 Ser Lys Asp Ala Pro Leu Val Ile Leu Tyr Gly Ser Pro Thr Glu Glu
178                195                200                205
180 ctg act aaa gat ttt ctt aaa ata ttg tat cca gat gca aag gct gga   3435
181 Leu Thr Lys Asp Phe Leu Lys Ile Leu Tyr Pro Asp Ala Lys Ala Gly
182                210                215                220
184 aaa tta aag ttt gta tgg agg tac att cca ctg gga atc aaa aaa ctg   3483
185 Lys Leu Lys Phe Val Trp Arg Tyr Ile Pro Leu Gly Ile Lys Lys Leu
186            225                230                235
188 gac tca att tct gga tac ggt gta tca ttg aaa atg gaa aag tat gat   3531
189 Asp Ser Ile Ser Gly Tyr Gly Val Ser Leu Lys Met Glu Lys Tyr Asp
190        240                245                250
192 tat tct ggt gca gaa gga aat cca aag tat gat ttg agt cga gat ttc   3579
193 Tyr Ser Gly Ala Glu Gly Asn Pro Lys Tyr Asp Leu Ser Arg Asp Phe
194 255                260                265                270
196 acc aga att aat gac tcg caa gag ttg gtc ctg gtc aat gaa aaa cat   3627
197 Thr Arg Ile Asn Asp Ser Gln Glu Leu Val Leu Val Asn Glu Lys His
198                275                280                285
200 tcg tat gaa ctt ggt gtt aaa ttg act tca ttc ata tta tcc aat cgt   3675
201 Ser Tyr Glu Leu Gly Val Lys Leu Thr Ser Phe Ile Leu Ser Asn Arg
202                290                295                300
204 tac aag agt act aaa tat gac ctt tta gat acg att tta acc aac ttt   3723
205 Tyr Lys Ser Thr Lys Tyr Asp Leu Leu Asp Thr Ile Leu Thr Asn Phe
206            305                310                315
208 ccc aag ttt att cct tac att gca cga tta cca aaa tta cta aat cat   3771
209 Pro Lys Phe Ile Pro Tyr Ile Ala Arg Leu Pro Lys Leu Leu Asn His
210        320                325                330
212 gaa aaa gtt aaa tcc aaa gtg ctt gga aat gaa gat ata ggg cta tct   3819
213 Glu Lys Val Lys Ser Lys Val Leu Gly Asn Glu Asp Ile Gly Leu Ser
214 335                340                345                350
216 caa gac tcc tac gga ata tat atc aac ggt tcc cca ata aat cca cta   3867
217 Gln Asp Ser Tyr Gly Ile Tyr Ile Asn Gly Ser Pro Ile Asn Pro Leu
218                355                360                365
220 gag tta gat att tac aat cta ggt acc agg ata aag gag gaa tta cag   3915
221 Glu Leu Asp Ile Tyr Asn Leu Gly Thr Arg Ile Lys Glu Glu Leu Gln
222                370                375                380
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224 act gtg aaa gat tta gtg aaa ctt gga ttt gat acc gta caa gca aag   3963
225 Thr Val Lys Asp Leu Val Lys Leu Gly Phe Asp Thr Val Gln Ala Lys
226         385                 390                 395
228 ctc ttg ata gca aaa ttt gct tta ctt tca gct gtt aaa caa aca caa   4011
229 Leu Leu Ile Ala Lys Phe Ala Leu Leu Ser Ala Val Lys Gln Thr Gln
230         400                 405                 410
232 ttt cga aat ggg aat aca tta atg ggt aac aat gaa aat aga ttt aaa   4059
233 Phe Arg Asn Gly Asn Thr Leu Met Gly Asn Asn Glu Asn Arg Phe Lys
234 415                 420                 425                 430
236 gtg tat gaa aat gaa ttt aag aag ggt agt tca gaa aag ggt ggg gtc   4107
237 Val Tyr Glu Asn Glu Phe Lys Lys Gly Ser Ser Glu Lys Gly Gly Val
238                 435                 440                 445
240 ttg ttt ttc aat aac att gaa tta gac aac aca ttc aag gag tac acc   4155
241 Leu Phe Phe Asn Asn Ile Glu Leu Asp Asn Thr Phe Lys Glu Tyr Thr
242         450                 455                 460
244 act gat cgt gag gag gca tat tta gga gtt ggt tct cat aaa ctt aag   4203
245 Thr Asp Arg Glu Glu Ala Tyr Leu Gly Val Gly Ser His Lys Leu Lys
246         465                 470                 475
248 cca aat caa att ccg tta ttg aaa gag aac atc cat gat tta att ttc   4251
249 Pro Asn Gln Ile Pro Leu Leu Lys Glu Asn Ile His Asp Leu Ile Phe
250         480                 485                 490
252 gca tta aat ttt ggg aac aaa aac caa ttg cgg gtg ttt ttc act tta   4299
253 Ala Leu Asn Phe Gly Asn Lys Asn Gln Leu Arg Val Phe Phe Thr Leu
254 495                 500                 505                 510
256 tct aag gtg att ttg gac tcc ggt ata cct caa caa gtt gga gtt ttg   4347
257 Ser Lys Val Ile Leu Asp Ser Gly Ile Pro Gln Gln Val Gly Val Leu
258                 515                 520                 525
260 ccc gtt ata gga gat gac cca atg gat ctg tta ctc gct gag aaa ttt   4395
261 Pro Val Ile Gly Asp Asp Pro Met Asp Leu Leu Leu Ala Glu Lys Phe
262                 530                 535                 540
264 tat tgg att gct gag aaa tca agc aca caa gag gca tta gca ata ttg   4443
265 Tyr Trp Ile Ala Glu Lys Ser Ser Thr Gln Glu Ala Leu Ala Ile Leu
266         545                 550                 555
268 tat aaa tat ttt gaa tca aac agt cca gat gaa gtt gat gac tta tta   4491
269 Tyr Lys Tyr Phe Glu Ser Asn Ser Pro Asp Glu Val Asp Asp Leu Leu
270         560                 565                 570
272 gat aaa gtg gaa gta ccc gaa gat tat aaa gtg gat tat aat cat gtg   4539
273 Asp Lys Val Glu Val Pro Glu Asp Tyr Lys Val Asp Tyr Asn His Val
274 575                 580                 585                 590
276 tta aac aag ttt tct ata tca act gct tcg gtc att ttc aat ggg gtt   4587
277 Leu Asn Lys Phe Ser Ile Ser Thr Ala Ser Val Ile Phe Asn Gly Val
278                 595                 600                 605
280 att tac gat tta aga gca cca aac tgg cag att gca atg agt aaa caa   4635
281 Ile Tyr Asp Leu Arg Ala Pro Asn Trp Gln Ile Ala Met Ser Lys Gln
282                 610                 615                 620
284 ata tcc cag gac att tca ctt att aaa act ttc ttg aga cag gga cca   4683
285 Ile Ser Gln Asp Ile Ser Leu Ile Lys Thr Phe Leu Arg Gln Gly Pro
286         625                 630                 635
288 ata gag ggt aga ttg aaa gat gtt ctt tac tct aat gca aaa tca gaa   4731
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289 Ile Glu Gly Arg Leu Lys Asp Val Leu Tyr Ser Asn Ala Lys Ser Glu
290     640                 645                 650
292 cgc aat tta cgt ata att cca tta gaa cct agt gac att att tac aag   4779
293 Arg Asn Leu Arg Ile Ile Pro Leu Glu Pro Ser Asp Ile Ile Tyr Lys
294 655                 660                 665                 670
296 aaa atc gac aag gaa tta ata aac aat tca att gca ttc aag aag cta   4827
297 Lys Ile Asp Lys Glu Leu Ile Asn Asn Ser Ile Ala Phe Lys Lys Leu
298             675                 680                 685
300 gat aaa gcg cag ggt gtg tct gga aca ttt tgg cta gtg tcg gat ttt   4875
301 Asp Lys Ala Gln Gly Val Ser Gly Thr Phe Trp Leu Val Ser Asp Phe
302             690                 695                 700
304 acc aag tca gca ata att act caa ttg ata gat ttg tta ttg ctt ctc   4923
305 Thr Lys Ser Ala Ile Ile Thr Gln Leu Ile Asp Leu Leu Leu Leu
306             705                 710                 715
308 aaa aag aaa gca att cag ata aga att att aat act ggg gat aca gat   4971
309 Lys Lys Lys Ala Ile Gln Ile Arg Ile Ile Asn Thr Gly Asp Thr Asp
310     720                 725                 730
312 gtt ttt gga aaa ttg aaa aca aag ttt aaa tta acc gcc tta aca aat   5019
313 Val Phe Gly Lys Leu Lys Thr Lys Phe Lys Leu Thr Ala Leu Thr Asn
314 735                 740                 745                 750
316 gga caa att gat gaa att att gag att ttg aaa aaa tcc aac gct tca   5067
317 Gly Gln Ile Asp Glu Ile Ile Glu Ile Leu Lys Lys Ser Asn Ala Ser
318             755                 760                 765
320 agt gca aat aat gat gaa ttg aaa aaa atg ctt gag act aag caa tta   5115
321 Ser Ala Asn Asn Asp Glu Leu Lys Lys Met Leu Glu Thr Lys Gln Leu
322             770                 775                 780
324 cct gct cat cac tct ttt ttg cta ttc aac tct aga tat ttt aga ttg   5163
325 Pro Ala His His Ser Phe Leu Leu Phe Asn Ser Arg Tyr Phe Arg Leu
326             785                 790                 795
328 gat gga aat ttt gga tac gag gaa ttg gat caa att ata gag ttt gaa   5211
329 Asp Gly Asn Phe Gly Tyr Glu Glu Leu Asp Gln Ile Ile Glu Phe Glu
330     800                 805                 810
332 gta tct caa aga ttg aac tta atc ccg gac atc atg gag gca tat ccg   5259
333 Val Ser Gln Arg Leu Asn Leu Ile Pro Asp Ile Met Glu Ala Tyr Pro
334 815                 820                 825                 830
336 gat gag ttt agg tcg aag aag gta agt gat ttt aat ctg gtt ttg tct   5307
337 Asp Glu Phe Arg Ser Lys Lys Val Ser Asp Phe Asn Leu Val Leu Ser
338             835                 840                 845
340 gga tta gac aat atg gac tgg ttt gat ttg gtg act tcc ata gtg aca   5355
341 Gly Leu Asp Asn Met Asp Trp Phe Asp Leu Val Thr Ser Ile Val Thr
342             850                 855                 860
344 aaa tca ttc cat gtc gac gaa aaa agg ttt att gtt gat gtt aac agg   5403
345 Lys Ser Phe His Val Asp Glu Lys Arg Phe Ile Val Asp Val Asn Arg
346             865                 870                 875
348 ttt gat ttt agc tca ttg gat ttt tca aac tcg att gat gta acg act   5451
349 Phe Asp Phe Ser Ser Leu Asp Phe Ser Asn Ser Ile Asp Val Thr Thr
350     880                 885                 890
352 tat gaa gaa aat agt cca gtt gat gta tta ata att ttg aac cct atg   5499
353 Tyr Glu Glu Asn Ser Pro Val Asp Val Leu Ile Ile Leu Asn Pro Met
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/13/2005
PATENT APPLICATION: US/10/018,105A   TIME: 16:17:31

Input Set : E:\substitute SEQLIST (10182-015-999).TXT
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 182,3408
Seq#:5; N Pos. 16,33,131,554,5240,5266,5293

VERIFICATION SUMMARY   DATE: 12/13/2005
PATENT APPLICATION: US/10/018,105A   TIME: 16:17:31

Input Set : E:\substitute SEQLIST (10182-015-999).TXT
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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:3383
L:1265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:120
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540
L:1568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:5238